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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=15; hr=18; min=27; sec=10; ms=270; ]

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Application No: 09866379 Version No: 1.0

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Total Errors: 0  
No. of SeqIDs Defined: 10  
Actual SeqID Count: 10

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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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# SEQUENCE LISTING

<110> Short, Jay M.  
 Kretz, Keith A.  
 Gray, Kevin A.  
 Barton, Nelson Robert  
 Garrett, James B.  
 O' Donoghue, Eileen  
 Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES  
 THEREOF

<130> 564462001822

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<141> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

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<150> US 09/259,214

<151> 1999-03-01

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5

10

15

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt	96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg	144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta	192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc	240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa	288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac	336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct	384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat	432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
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Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac	528
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
195 200 205	
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Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
210 215 220	
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	
225 230 235 240	
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Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
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gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
260	265 270
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
275	280 285
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His	
290	295 300
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu	
305	310 315 320
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
325	330 335
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Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340	345 350
ggg gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355	360 365
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
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aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385	390 395 400
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405	410 415
ggg ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
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Arg Ser His His His His His His	
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Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
35 40 45  
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
50 55 60  
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
65 70 75 80  
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
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Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
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Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
115 120 125  
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165 170 175  
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
180 185 190  
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu  
195 200 205  
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
210 215 220  
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
225 230 235 240  
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
245 250 255  
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
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Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
305 310 315 320  
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Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
355 360 365  
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
370 375 380  
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
385 390 395 400  
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
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160 165 170

gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
gtg ctt aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag	805
Val Leu As	